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Supplemental Material

Evaluating the Effect of Gestational Exposure to Perfluorohexane Sulfonate on Placental Development in Mice Combining Alternative Splicing and Gene Expression Analyses

Yihao Zhang, Jia Lv, Yi-Jun Fan, Lin Tao, Jingjing Xu, Weitian Tang, Nan Sun, Ling-Li Zhao, De-Xiang Xu, and Yichao Huang

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Figure S2. The distribution of core genes in GSEA. (A) The distribution of core genes in GSEA for placenta development. (B) The distribution of core genes in GSEA for multicellular organism metabolic process. (C) The distribution of core genes in GSEA for anion transmembrane transport. N = 6 in each group, including 3 males and 3 females. P and FDR values were determined by permutation test and Benjamini-Hochberg method, respectively. Data in (A-C) are also presented in Excel Table S19. Notes: FDR, false discovery rate; GO, Gene Onotology; GSEA, gene set enrichment analysis; PFHxS, perfluorohexane sulfonate.

Figure S3. Signal pathways in multiple biological processes of placental development in response to PFHxS exposure. (A) Heatmap showing the DEGs profile of development gene set between high-dose group and control. (B) Heatmap showing the DEGs profile of metabolic process gene set between high-dose group and control. (C) Heatmap showing the DEGs profile of proliferation gene set between high-dose group and control. (D) Heatmap showing the DEGs profile of transport gene set between high-dose group and control. (E) GSEA showing the positive enrichment of TGF β signaling pathway in high-dose group compare to control. (F) GSEA showing the positive enrichment of p53 signaling pathway in high-dose group compare to control. (G) GSEA showing the positive enrichment of Wnt signaling pathway in high-dose group compare to control. (H) UpSetR plot showing the number of unique and shared DEGs between development, proliferation, metabolic process and transport gene sets. (I) Circos plot showing GO analysis of shared DEGs for 4 gene sets. N = 6 in each group, including 3 males and 3 females. Pand FDR values were determined by permutation test and Benjamini-Hochberg method (E, F and G), respectively. Data in (A-I) are also presented in Excel Table S20. Notes: DEGs, differentially expressed genes; FDR, false discovery rate; GSEA, gene set enrichment analysis; PFHxS, perfluorohexane sulfonate.

Figure S4. AS analyses in multiple signal pathways of metabolism and transport after PFHxS exposure. (A) The number of differential AS events in male placenta with PFHxS expose compare to control. (B) The number of differential AS events in female placenta with PFHxS expose compare to control. (C) The proportion of differential AS events in male and female placenta with PFHxS expose compare to control. (D) GO analysis showing the genes with AS event are enriched in multiple signal pathways of metabolism and transport in male placenta. (E) GO analysis showing the genes with AS event are enriched in multiple signal pathways of metabolism and transport in female placenta. (F) Heatmap showing the profile of splicing factors in male and female placenta with PFHxS expose compare to control. N = 6 in each group, including 3 males and 3 females. P values were determined by hypergeometric test (D and E). Data in (A-F) are also presented in Excel Table S21. Notes: AS, alternative splicing; GO, Gene Onotology; PFHxS, perfluorohexane sulfonate.

Figure S5. AS analyses in multiple signal pathways of placental development after PFHxS exposure. (A) KEGG pathway interaction analysis showing the relationship between signal pathways in RI gene set. (B) KEGG pathway interaction analysis showing the relationship between signal pathways in A3SS gene set. (C) KEGG pathway interaction analysis showing the relationship between signal pathways in A5SS gene set. (D) KEGG pathway interaction analysis showing the relationship between signal pathways in SE gene set. (E) KEGG pathway interaction analysis showing the relationship between signal pathways in MXE gene set. (F) Reactome analysis showing the genes with AS event are enriched in multiple signal pathways related to placental development. *N* = 6 in each group, including 3 males and 3 females. *P* values were determined by hypergeometric test (F). Data in (A-F) are also presented in Excel Table S22. Notes: A3SS, alternative 3'plice site; A5SS, alternative 5'plice site; AS, alternative splicing; KEGG, Kyoto Encyclopedia of Genes and Genomes; MXE, exclusion exon; SE skipped exon; PFHxS, perfluorohexane sulfonate; RI, retained intron.

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Additional File- Excel Document

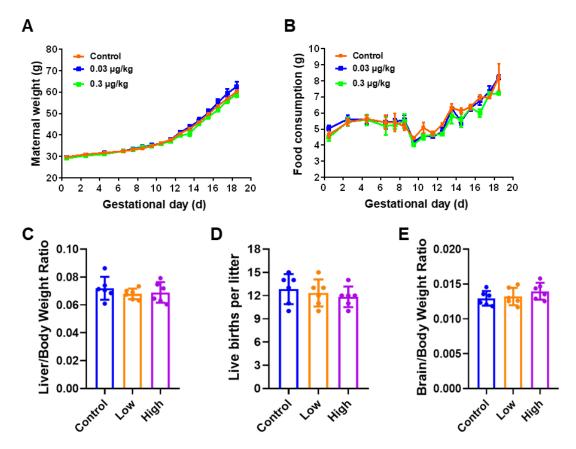


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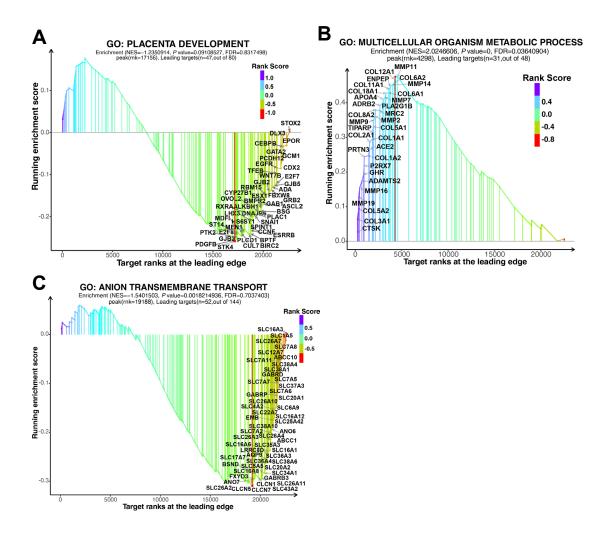
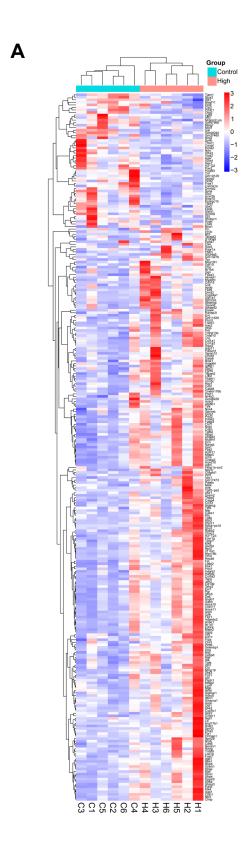
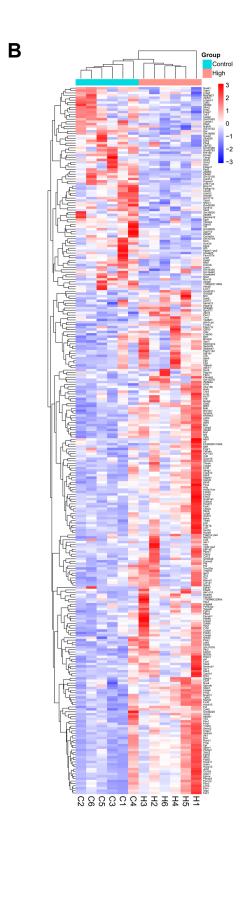
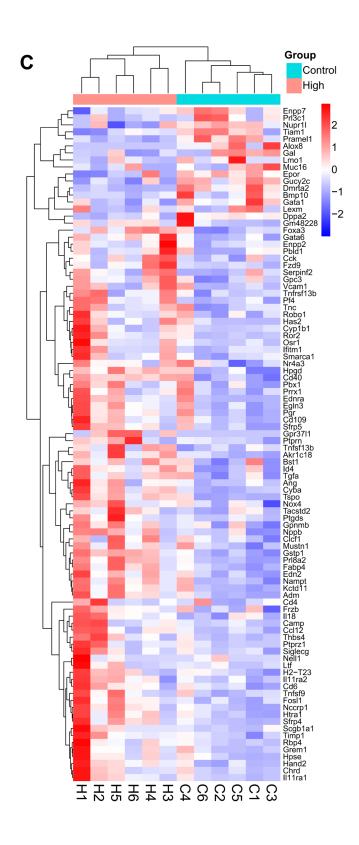
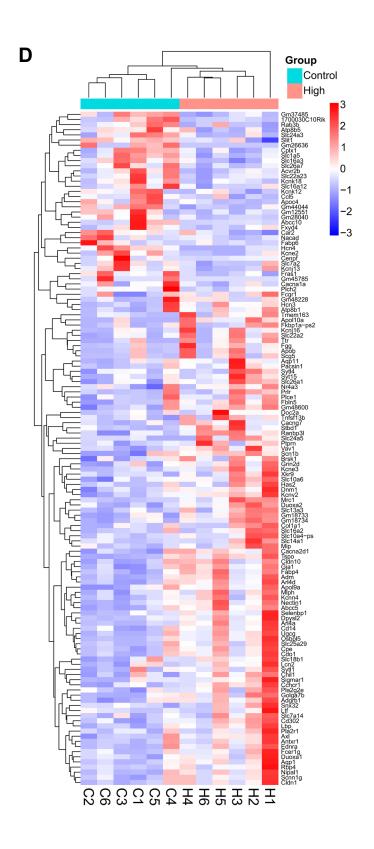


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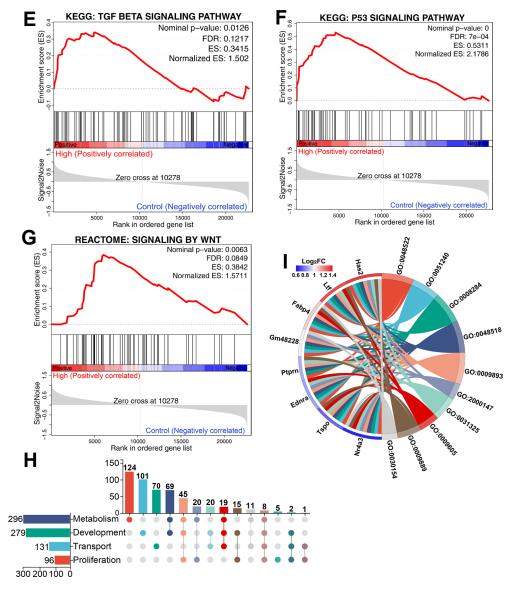


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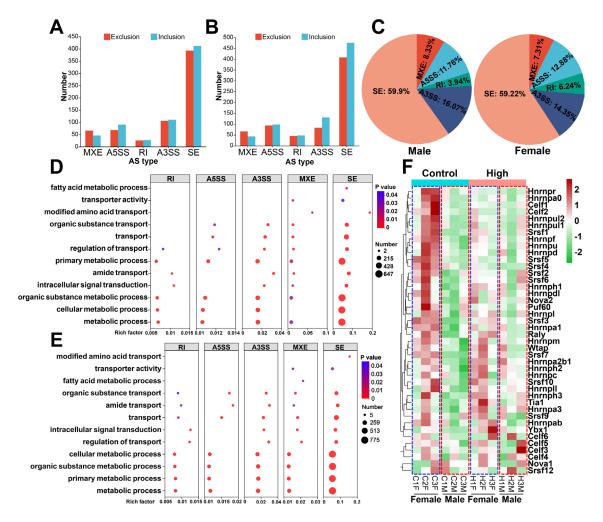
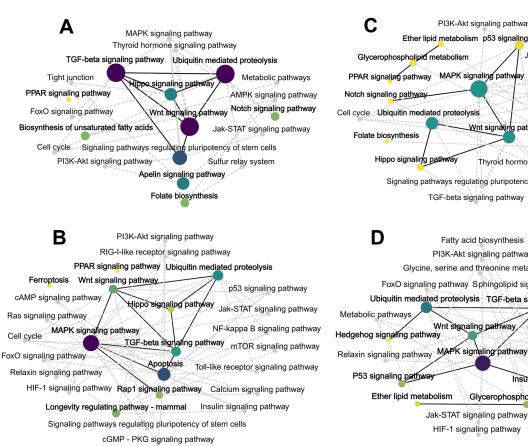


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Rap1 signaling pathway E Phospholipase D signaling pathway AGE-RAGE signaling pathway in diabetic complications Jak-STAT signaling pathway Apoptosis AMPK signaling pathway Estrogen signaling pathway

TGF-beta signaling pathway

Cell cycle

Notch signaling pathway

CGMP - PKG signaling cGMP - PKG signaling pathway FoxO signaling pathway Relaxin signaling pathway Wnt signaling pathway MAPK signaling pathway Ubiquitin mediated proteolysis PPAR signaling pathway Metabolic pathways Ras signaling pathway thways egulating pluripotency of stem cells Nicotinate and nicotinamide metabolism Insulin signaling pathway ErbB signaling pathway PI3K-Akt signaling pathway HIF-1 signaling pathway NF-kappa B signaling pathway Apelin signaling pathway VEGF signaling pathway Biosynthesis of unsaturated fatty acids p53 signaling pathway Hippo signaling pathway Sphingolipid signaling pathway

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Sphingolipid metabolism

Insulin signaling pathway

Glycerophospholipid metabolism

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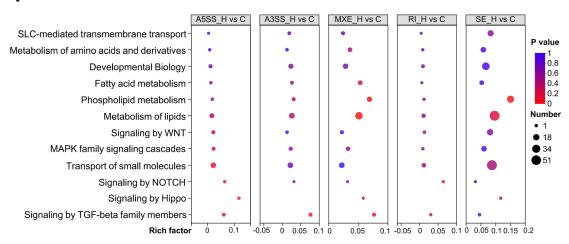


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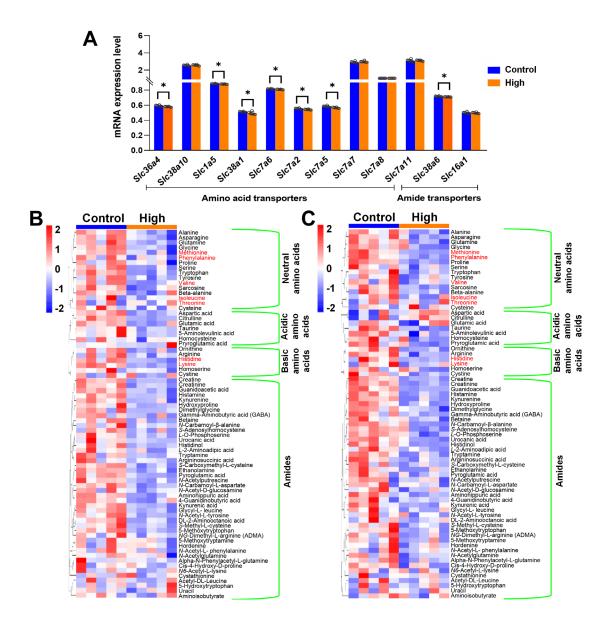


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